

SEQUENCE LISTING

<110> NIPPON MEDICAL SCHOOL FOUNDATION

<120> Cell death-inducing fusion gene specifically acting on cancer and  
gene product thereof

<130> PH-2011-PCT

<140>

<141>

<150> JP2003/081337

<151> 2003-03-24

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (579)

<400> 1

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Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser

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gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag				96
Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln				
20	25	30		
gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac				144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp				
35	40	45		
ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag				192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys				
50	55	60		
cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att				240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile				
65	70	75	80	
gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca				288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala				
85	90	95		
gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc				336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala				
100	105	110		
ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag				384
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys				
115	120	125		

gtg ccg gaa ctg atc aga acc atc atg ggc tgg aca ttg gac ttc ctc 432  
 Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu  
 130 135 140

cgg gag cgg ctg ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc 480  
 Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly  
 145 150 155 160

ctc ctc tcc tac ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt 528  
 Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe  
 165 170 175

gtg gcg gga gtg ctc acc gcc tcg ctc acc atc tgg aag aag atg ggc 576  
 Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly  
 180 185 190

tga 579

<210> 2

<211> 192

<212> PRT

<213> Homo sapiens

<400> 2

Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser  
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 20 25 30  
 Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp

	35	40	45
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys			
50	55	60	
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile			
65	70	75	80
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala			
	85	90	95
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala			
100	105	110	
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys			
115	120	125	
Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu			
130	135	140	
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly			
145	150	155	160
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe			
	165	170	175
Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly			
180	185	190	

<210> 3

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (999)

<400> 3

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Met Ala Cys Asp Cys Arg Gly Asp Cys Phe Cys Gly Gly Met Ser Lys  
1 5 10 15

ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat 96  
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp  
20 25 30

ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt 144  
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly  
35 40 45

gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc act gga 192  
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly  
50 55 60

aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc acc tat ggc 240  
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly  
65 70 75 80

gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat gac ttt 288  
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe  
85 90 95

ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc atc ttt 336  
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe  
100 105 110

ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa 384  
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu  
115 120 125

ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac ttt aag 432  
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
130 135 140

gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat aac tcc 480  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
145 150 155 160

cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc aag gtc 528  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
165 170 175

aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag ctg gcc 576  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
180 185 190

gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg ctc ctc 624  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
195 200 205

cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc 672  
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
210 215 220

aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc gct gct 720  
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala

225

230

235

240

ggg atc aca cat ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt 768

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe

245

250

255

gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg 816

Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu

260

265

270

atc aga acc atc atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg 864

Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu

275

280

285

ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac 912

Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr

290

295

300

ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg 960

Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val

305

310

315

320

ctc acc gcc tca ctc acc atc tgg aag aag atg ggc tga

999

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly

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330

<210> 4

<211> 332

<212> PRT

<213> Homo sapiens

<400> 4

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20 25 30  
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly  
35 40 45  
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly  
50 55 60  
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly  
65 70 75 80  
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe  
85 90 95  
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe  
100 105 110  
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu  
115 120 125  
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
130 135 140  
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser  
145 150 155 160  
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val  
165 170 175  
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
180 185 190  
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
195 200 205  
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
210 215 220



Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 225                      230                      235                      240  
 Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe  
                          245                      250                      255  
 Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu  
                          260                      265                      270  
 Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu  
                          275                      280                      285  
 Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr  
                          290                      295                      300  
 Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val  
 305                      310                      315                      320  
 Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly  
                          325                      330

<210> 5

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(987)

<400> 5

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Met Ala Cys Asn Gly Arg Cys Gly Gly Met Ser Lys Gly Glu Glu Leu

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15

ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat	96
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn	
20 25 30	
ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt gat gcc aca tac	144
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr	
35 40 45	
gga aag ctc acc ctg aaa ttc atc tgc acc act gga aag ctc cct gtg	192
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
50 55 60	
cca tgg cca aca ctg gtc act acc ttc acc tat ggc gtg cag tgc ttt	240
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe	
65 70 75 80	
tcc aga tac cca gac cat atg aag cag cat gac ttt ttc aag agc gcc	288
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala	
85 90 95	
atg ccc gag ggc tat gtg cag gag aga acc atc ttt ttc aaa gat gac	336
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
100 105 110	
ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg	384
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
115 120 125	
gtg aat aga atc gag ctg aag ggc att gac ttt aag gag gat gga aac	432
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn	

130	135	140	
att ctc ggc cac aag ctg gaa tac aac tat aac tcc cac aat gtg tac			480
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
145	150	155	160
atc atg gcc gac aag caa aag aat ggc atc aag gtc aac ttc aag atc			528
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
	165	170	175
aga cac aac att gag gat gga tcc gtg cag ctg gcc gac cat tat caa			576
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
	180	185	190
cag aac act cca atc ggc gac ggc cct gtg ctc ctc cca gac aac cat			624
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
	195	200	205
tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc aac gaa aag aga			672
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
	210	215	220
gac cac atg gtc ctg ctg gag ttt gtg acc gct gct ggg atc aca cat			720
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His			
225	230	235	240
ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt gcc agc aaa ctg			768
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu			
	245	250	255

gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg atc aga acc atc 816  
 Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile  
 260 265 270

atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg ttg ggc tgg atc 864  
 Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile  
 275 280 285

caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac ttt ggg acg ccc 912  
 Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro  
 290 295 300

acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg ctc acc gcc tca 960  
 Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser  
 305 310 315 320

ctc acc atc tgg aag aag atg ggc tga 987  
 Leu Thr Ile Trp Lys Lys Met Gly  
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<210> 6

<211> 328

<212> PRT

<213> Homo sapiens

<400> 6

Met Ala Cys Asn Gly Arg Cys Gly Gly Met Ser Lys Gly Glu Glu Leu  
 1 5 10 15  
 Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn

	20	25	30
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr			
35	40	45	
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
50	55	60	
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe			
65	70	75	80
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala			
85	90	95	
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
100	105	110	
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
115	120	125	
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
130	135	140	
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr			
145	150	155	160
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile			
165	170	175	
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln			
180	185	190	
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His			
195	200	205	
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg			
210	215	220	
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His			
225	230	235	240
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu			
245	250	255	
Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile			

260	265	270
Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile		
275	280	285
Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro		
290	295	300
Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser		
305	310	315
Leu Thr Ile Trp Lys Lys Met Gly		320
325		

<210> 7

<211> 9

<212> PRT

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<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 7

Cys Leu Ser Ser Arg Leu Asp Ala Cys

1 5

<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 8

Cys Asn Ser Arg Leu His Leu Arg Cys

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5

<210> 9

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

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Cys Glu Asn Trp Trp Gly Asp Val Cys

1

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<210> 10

<211> 21

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 10

Trp Arg Cys Val Leu Arg Glu Gly Pro Ala Gly Gly Cys Ala Trp Phe

1

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10

15

Asn Arg His Arg Leu

20

<210> 11

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 11

Cys Leu Pro Val Ala Ser Cys

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<210> 12

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 12

Cys Gly Ala Arg Glu Met Cys

1

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<210> 13

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 13

Cys Lys Ser Thr His Asp Arg Leu Cys

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<210> 14

<211> 9

<212> PRT

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<223> Description of Artificial Sequence:Homing peptide

<400> 14

Cys Gly Asn Lys Arg Thr Arg Gly Cys

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<210> 15

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 15

Ala Pro Arg Pro Gly

1 5

<210> 16

<211> 6

<212> PRT

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<223> Description of Artificial Sequence:Homing peptide

<400> 16

Lys Gln Ala Gly Asp Val

1 5

<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 17

Lys Arg Leu Asp Gly Ser

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<210> 18

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 18

Asp Gly Glu Ala

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<210> 19

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

<220>

<221> misc\_feature

<222> (1).. (2)

<223> n is A, C, G or T

<400> 19

nnatcgatcc accatgagca agggcgag

28

<210> 20

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 20

ctggcaaagt agaaaagggc cttgtacagc tcgtc

35

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 21

gcccttttct actttgccag

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<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<221> misc\_feature

<222> (1).. (2)

<223> n is A, C, G or T

<400> 22

nntctagatc agcccatctt cttcca

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<210> 23

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 23

ccatggcctg cgattgccgt ggtgattgtt tttgtggtgg tatgagcaag ggcgagg

57

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> misc\_feature

<222> (1)..(4)

<223> n is A, C, G or T

<400> 24

nnnnccatgg cctgcgattg cc

22

<210> 25

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 25

tggaagca ctgcacgc

18

<210> 26

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 26

ccatggcctg caacggctgt tgcggtggta tgagcaaggg cgagg

45

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> misc\_feature

<222> (1)..(4)

<223> n is A, C, G or T

<400> 27

nnnnccatgg cctgcaacgg tc

22